

best Local Similarity: 85.19% Mismatches: 0
Query Match: 81.68% Indels: 20
B: 9 Gaps: 1

S-10-005-907-2 (1-135) x AK126682 (1-4032)

1 MethylaspartylleuGluAspSerCysLeuGlyGluAsnGlyLysProlys 20
377 ATGGGATTCTCTGGAAACT..... 403

21 LeuGlyAsnProAspGluGluArglyBrglGlnGluMetThrPheGluArglyBrgl 40
404-AGCAGGAACTGACTACATTGAAAGAACT 436

41 CysAspGlnAspLysSerGluSerGluSerGlnGluAsnGluAsn 60
437 CAGAAAGAAAGCCGAGAGTCGAGGTTCACTCTTCACTGAAACCGAACT 496

CDS

61 GlyserLysSerGluGluValCysGlyThrValleAbhrIleProHsGlnArgSer 80
497 GCGACTGTTGTTGTCAGAGAGTGTCTACAGTCTTACATGAGATCC 556

81 SerLeuSerSerAsnAspGlyTyrGluAsnIleAspSerLeuThrArglyValArg 100
557 TCCCTGAGCTGAGCTCATGATGATGATGATGATGAGACATGATGCTCAGAGA 616

101 GluPheArgGluArgSerGluLysGluGluSerGlnSerValAspPro 120
617 CAGTTAGAGAAAGTCAGACAGATAATCCCTCTAGGACTTCGTTAGCCCT 676

121 CysSerCysThrHisGluIleAspPheGluValValPheProHis 135
677 TGTTCCTGAGCCATCAGCAGTCAGTGTGTTGACAC 721

RESULT 6

AK124520 4136 bp mRNA linear PRI 09-SEP-2003
AK124520 Home sapiens cDNA FLJ42559 fib, clone BRACE302390.

DEFINITION
VERSION AK124520.1 GI:34530324
KEYWORDS Oligo capping, fib (Full insert sequence).
SOURCE Home sapiens (human)
ORGANISM Home sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, M., Yamazaki, M.,
Kambara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Ito, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hiro, Y., Saito, K., Nishikawa, T.,
Kumada, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sezine, M.,
Kikuchi, H., Murakawa, K., Kaneko, K., Takahashi, Fujii, A.,
Oshimura, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagamatz, K., Matsuo, Y., Nagai, K., and Iroga, T.

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4136)
AUTHORS Nagai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
COMMENT Kazusa-Komatsui, Kisarazu, Chiba 292-0818, Japan
(E-mail):genomicshri.co.jp, Tel:81-438-52-3975, Fax: 81-438-52-3986
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

JOURNAL
REFERENCE source
FEATURES source
QUALIFIERS 1. 4136

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41 CysAspGlnAspLysSerGluSerGluSerGlnGluAsnGluAsn 60
437 CAGAAAGAAAGCCGAGAGTCGAGGTTCACTCTTCACTGAAACCGAACT 496

CDS

61 GlyserLysSerGluGluValCysGlyThrValleAbhrIleProHsGlnArgSer 80
497 GCGACTGTTGTTGTCAGAGAGTGTCTACAGTCTTACATGAGATCC 556

81 SerLeuSerSerAsnAspGlyTyrGluAsnIleAspSerLeuThrArglyValArg 100
557 TCCCTGAGCTGAGCTCATGATGATGATGATGAGACATGATGCTCAGAGA 616

101 GluPheArgGluArgSerGluLysGluGluSerGlnSerValAspPro 120
617 CAGTTAGAGAAAGTCAGACAGATAATCCCTCTAGGACTTCGTTAGCCCT 676

121 CysSerCysThrHisGluIleAspPheGluValValPheProHis 135
677 TGTTCCTGAGCCATCAGCAGTCAGTGTGTTGACAC 721

RESULT 7

AC074365 141268 bp DNA clone 3711-11574, linear HTG 22-SEP-2000

DEFINITION Home sapiens chromosome 1 clone 3711-11574, WORKING DRAFT SEQUENCE

ACCESSION AC074365
VERSION AC074365.5 GI:10280935
KEYWORDS HTG, HTGS, PRASE1, HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; 1. bases 1 to 141268;
Natters, R.H. The sequence of Homo sapiens clone
Unpublished 2 (bases 1 to 141268)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
REFERENCE
TITLE
JOURNAL
COMMENT
REFERENCE
TITLE
JOURNAL
COMMENT
FEATURES source

Location/Qualifiers

Mamm. Genome 13 (8), 475-478 (2002)

FEATURES source

1. 527 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9605"
 /clone="MRCB:109064"
 /tissue_type="from acute myelogenous leukemia"
 /lab_host="DHLIB (M1 phage-resistant)"
 /cln_line="NIH MGC 55"
 /note="Organ: bone marrow; Vector: PDMR-LIB (Clontech);
 Site 1: SfI (ggccgcctccggcc); Site 2: SfI
 (ggccattatggcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' - digester sequence: 5'-CACGGCCATTCGGCC-3' and
 3' - adaptor sequence: 5'-ATTCTAGAGCCAGGGGCCatATG-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.85 kb (range 0.9-4.0 kb). 14/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

ORIGIN

Query Match 100.0%; Score 405; DB 10; Length 527;
 Best Local Similarity 100.0%; Pred. No. 6.1e-86;
 Matches 405; Conservative 0; Mismatches 0; Indels 0; GAPS 0;
 Qy 1 ATGGAAATTAATCTCGGCAAACTGAGTGTGGAGGAACTGGCCAG 60
 Db 45 ATGGAAATTAATCTCGGAAAACTCACTGGCTGGAGGAACTGGCCAG 104
 Qy 61 RANGGAACCCGATAGGGAGGAAACGGCAGGAATGACATTTGAAAGAACTT 120
 Db 105 RANGGAACCCGATAGGGAGGAAACGGCAGGAATGACATTTGAAAGAACTT 164
 Qy 121 CAGATCAAGATAAGAAACGCCAGAAGTTCTCAATCAGAAACGAGAT 180
 Db 165 CAGATCAAGATAAGAAACGCCAGAAGTTCTCAATCAGAAACGAGAT 224
 Qy 181 GGCAGTGTTCTCGAAGAGGTGTACAGTGCTTATCATACATCCCATAGAGATC 240
 Db 225 GGCAGTGTTCTCGAAGAGGTGTACAGTGCTTATCATACATCCCATAGAGATC 284
 Qy 241 TCCCTGAGCTCCATGATGAGGTGTAGGAACTCTCAGAAAGTGAGA 300
 Db 285 TCCCTGAGCTCCATGATGAGGTGTAGGAACTCTCAGAAAGTGAGA 344
 Qy 301 CAGTTAGGAAAGGTGAGGAGCATGAGATAATGAGGTTGTTGAGGCT 360
 Db 345 CAGTTAGGAAAGGTGAGGAGCATGAGATAATGAGGTTGTTGAGGCT 404
 Qy 361 TATTCCTGGACCATGAGCATGATGAGGTTGTTGTTGAGGTTGTTGAGC 405
 Db 405 TATTCCTGGACCATGAGCATGATGAGGTTGTTGTTGAGGTTGTTGAGC 449

JOURNAL
 MBLINE
 PUBMED
 COMMENT

Smith TPL, US Meat Animal Research Center

DC Box 166, Clay Center, NE 68933-0166, USA

Fax: 402 762 4366

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
 v0.98904.e. Vector identified by cross_match with the -minscore 20
 and -minmatch 12 options.

PCR Primers
 FORWARD: AGGAAACAGCTATGACCTACCAT
 BACKWARD: GTTTCAGCCAGTCGAGCGPlace: 19 row: F column: 21
 Seq primer: ATTAGGGATACATAPAG.

Location/Qualifiers

1. 288

/organism="Sus scrofa"

/mol_type="mRNA"

/tissue_type="pool"

/lab_host="DHLIB"

/clone="MRC 2PIG"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: Sall; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

FEATURES source

ORIGIN

Query Match 15.0%; Score 64.8; DB 10; Length 288;
 Best Local Similarity 75.8%; Pred. No. 4e-05;
 Matches 94; Conservative 0; Mismatches 27; Indels 3; GAPS 1;
 Qy 285 CCAAGGAGATGAGACATTTGAGAAGGTGAGAGAAATAGGCCTCTTGGAC 344
 Db 2 CACAAAGGAGATGAGACATTTGAGAAGGTGAGAGAAATAGGCCTCTTGGAC 61
 Qy 345 TCTGTGATGTTAGCTTCTCGACCCATGAGCATGATGAGTGTGTTGTC 401
 Db 62 GACTTACATCCAAAGTTCTTCTTATACCCCTGAGAATGATTGACTGCTTC 121
 Qy 402 ACAC 405
 Db 122 TCAC 125

RESULT 3
 BP797507 LOCUS BP797507
 DEFINITION 60225174P1_NTH_MGC_85 Homo sapiens mRNA sequence.
 ACCESSION BP797507
 VERSION BP797507.1 GI:12102561
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Batareya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Batareya; Butharia; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1045)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: cgbab@mail.nih.gov

Tissue Procurement: Louis Straub, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (I.M.N.L)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/I.M.N.L at:

http://image1.mgi.org/

Plate: L1A952 row: d column: 20

REFERENCE 1 (bases 1 to 288)
 AUTHORS Fahrenkrug, S.C., Smith, T.P.L., Prokopi, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Perna, G., Sultana, R., Quackenbush, J., and Keeler, J.W.

TITLE Porcine gene discovery by normalized cDNA library sequencing and EST cluster assembly

Yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butheria; Primates; Catarrhini; Hominidae; Homo.

Eukaryotic
Mammals

FEATURES

Source

1. 527
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db="2"
 /db_xref="taxon:9606"
 /clone="IMAGE:4109064"
 /tissue_type="acute myelogenous leukemia"
 /lab_hora="DH10B (T1 phage-resistant)"
 /clone_lib="NTH MGC_55"
 /note="Organ: bone marrow; Vector: PDR-LIB (Clontech);
 Site 1: SfiI (Ggcgcctggcc); Site 2: SfiI
 (Ggcattatggcc); Double-stranded cDNA was prepared from
 cell line 293NA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CAGGCCATATGACC-3' and
 3' adaptor sequence:
 5'-ATGAGGCGAGGGCGAGGAGATG-3' (3'BN-3' (where B = A,
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 1.65 kb. Average 0.9-4.0 kb. 14/15 colonies contained
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Query Match Similarity 100.0%; Score 405; DB 10; Length 527;
 Best Local Similarity 100.0%; Red. No. 6.1e-86; Length 527;
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 Qy 1 ATGGAAATTCTCTCCGAAACAACTCGTCTGGCGATGATGAGGCCAAG 60
 Db 45 ATGGAAATTCTCTCCGAAACAACTCGTCTGGCGATGATGAGGCCAAG 104
 Qy 61 AAGGAAACCCATGAGGAAAGAAACGGCAAGAAATGACTCATTTGAGAAACT 120
 Db 105 AAGGAAACCCATGAGGAAAGAAACGGCAAGAAATGACTCATTTGAGAAACT 164
 Qy 121 CAGATCAAGTATGAAAGCAGAGTGTTCATCTCTATTCAGAAACGAGAT 180
 Db 165 CAGATCAAGTATGAAAGCAGAGTGTTCATCTCTATTCAGAAACGAGAT 224
 Qy 181 GCGAGTGGTTGTGAGAGTGTGTAGCTGCTTAATCACATCCCTATGAGATCC 240
 Db 225 GCGAGTGGTTGTGAGAGTGTGTAGCTGCTTAATCACATCCCTATGAGATCC 284
 Qy 241 TCCTAGTCAATGATGATGGTTAGACATGACTCTCTCAAGGAAGTGA 300
 Db 285 TCCCTGAGTCATGATGAGGCTATGAGACATGAGACATGAGACATGAGA 344
 Qy 301 CAGTTAGAGAGTCAGAGCAATGAGCAATGAGCTCTAGACTCTGTAGGCT 360
 Db 345 CAGTTAGAGAGTCAGAGCAATGAGCAATGAGCTCTAGACTCTGTAGGCT 404
 Qy 361 TGTTCCTGACCCATGAGCATATGAGCTGTTCACAC 405
 Db 405 TGTTCCTGACCCATGAGCATATGAGCTGTTCACAC 449

RESULT 2

AW180906 33516 MARC 2PIG Sub scrofa mRNA 288 bp linear ~~EST 09-JUL-2000~~
 LOCUS mRNA sequence
 DEFINITION Sub scrofa
 ACCESSION AW180906
 VERSION AW180906.1 GI:7050949
 KEYWORDS EST
 SOURCE Sub scrofa (pig)
 ORGANISM Bivalvia; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheroidea; Cephalopoda; Rodentia; Suina; Suidae; Subs.
 REFERENCE 1 (bases 1 to 288)
 AUTHORS Fahrnkraus, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
 Waller, J., Wiegert, R., Rohrer, G.A., Petrea, G., Sultana, R.,
 Quackenbush, J., and Keele, J.W.
 TITLE Porcine gene discovery by normalized cDNA-library sequencing and
 EST cluster assembly